

REMARKS

Status of the Claims

Claims 1-48 are currently pending. Claims 1-17 and 19-40 are withdrawn from further consideration in response to a restriction requirement by the Examiner, under 37 C.F.R. §1.142(b).

In the present Response, claims 1-17 and 19-40 are cancelled; claim 18 is amended; and claims 49-71 are added. Thus, after entry of these amendments, claims 18 and 41-71 are presented for reconsideration.

Support for the Claim Amendments

Support for new independent claim 56 and dependent claims 57-64, directed to nucleic acid sequences encoding the enzyme of FIG 1, SEQ ID NO:2, can be found, *inter alia*, at page 22, lines 27-30; and page 23, lines 9-13, of the specification. Support for new claims 49 and 62 directed to liberation of inorganic phosphates prior to ingestion of the foodstuff can be found, *inter alia*, at page 10, lines 11-17. Support for new claims 50 and 66 directed to purifying the expressed polypeptide can be found, *inter alia*, at page 63, lines 13-17. Support for new claims 51 and 67 can be found, *inter alia*, at page 63, lines 18-19. Support for new claims 52 and 68 directed to feed for non-ruminant animals can be found, *inter alia*, at page 7, lines 21-32. Support for new claims 53 and 69 directed to feed for monogastric animals can be found, *inter alia*, at page 5, lines 30-32. Support for new claims 54 and 70 directed to dicotyledonous species can be found, *inter alia*, at page 63, line 31, to page 63, line 1; and page 66, lines 8-17. Support for new claims 55 and 71 directed to monocotyledonous species can be found, *inter alia*, at page 66, line 19, to page 67, line 7. Accordingly, Applicants submit that no new matter has been introduced by the present amendments.

Objections to the Specification

The specification is objected to as containing an embedded hyperlink and/or other form of browser-executable code. The instant amendment overcomes this objection.

The specification is objected to for not having updated status information of non-provisional applications 09/318,528, 09/291,931, and 09/259,214. The instant amendment overcomes this objection.

Applicants submit no new matter has been introduced by the instant amendments. In light of the above referenced amendments, Applicants respectfully request withdrawal of the objections to the specification.

Objections to the Oath/Declaration

The Oath/Declaration has been found defective because no date is next to the signature of the inventor, Jay Short. Applicants submit herewith a new declaration signed and dated by Jay Short. Applicants aver that the new declaration overcomes the objection to the Oath/Declaration and request withdrawal of the objection.

Issues under 35 U.S.C. §112, second paragraph

Independent claim 18 and dependent claims 41-48 are rejected under 35 U.S.C. 112, second paragraph, for allegedly being indefinite for reciting the phrase "preparing a plant cell, plant part, or plant that contains a recombinant expression system." It is alleged that it is unclear what the meaning of the word "preparing" is within the context of the claim since the plant cell, plant part, or plant has already been transformed with the DNA encoding the phytase of SEQ ID NO:2, the term "prepare" cannot be associated with "transform."

Applicants have amended claim 18 to clarify the method for producing an animal feed to comprise providing a plant cell, plant part or plant that contains a recombinant expression system. As the Patent Office has pointed out, the plant cell, plant part, or plant has already been transformed with the DNA encoding the phytase of SEQ ID NO:2, exemplary methods are

provided in the specification (*e.g.*, see page 65, line 28, to page 66, line, 6). Accordingly, the claimed method recites providing the transformed plant cell, plant part, or plant, culturing them, and converting them into a composition suitable for animal feed.

Applicants respectfully submit that amended claims 18 and 41-48 are patentable.

CONCLUSION

Claims 18 and 41-48 are pending in the application. Claim 18 has been amended by the present Response. Applicants request that the Examiner reconsider the application and claims in light of the foregoing reasons and amendments and respectfully submit that the claims are in condition for allowance.

If, in the Examiner's opinion, a telephonic interview would expedite the favorable prosecution of the present application, the undersigned attorney would welcome the opportunity to discuss any outstanding issues and to work with the Examiner toward placing the application in condition for allowance.

Attached is a marked-up version of the changes being made by the current amendment.

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Applicants believe that no fees are necessitated by the present Response. However, in the event any fees are due, the Commissioner is hereby authorized to charge any such fees to Deposit Account No. 06-1050.

Respectfully submitted,

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Mi K. Kim
Mi K. Kim
Reg. No. 44,830

Fish & Richardson P.C.
PTO Customer Number 20985
4350 La Jolla Village Drive, Suite 500
San Diego, California 92122
Telephone: (858) 678-5070
Facsimile: (858) 678-5099
10200477.doc

Version with markings to show changes made

In the specification:

Paragraph beginning at page 1, line 4 has been amended as follows:

This application is a continuation-in-part of U.S. Patent Application Serial No. 09/318,528, filed May 25, 1999, which is a continuation-in-part of U.S. Patent Application Serial No. 09/291,931, now U.S. Patent No. 6,190,897, filed April 13, 1999, which is a continuation of U.S. Patent Application Serial No. 09/259,214, now U.S. Patent No. 6,110,719, filed March 1, 1999, which is a divisional of U.S. Patent Application Serial No. 08/910,798, now U.S. Patent No. 5,876,997, filed August 13, 1997, all of which are hereby incorporated by reference in their entirety.

Paragraph beginning at page 24, line 29 has been amended as follows:

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443, 1970, by the search for similarity method of person & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool),

BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project [(J. Roach, http://weber.u.Washington.edu/~roach/human_genome_progress2.html)] (Gibbs, 1995). At least twenty-one other genomes have already been sequenced, including, for example, *M. genitalium* (Fraser *et al.*, 1995), *M. jannaschii* (Bult *et al.*, 1996), *H. influenzae* (Fleischmann *et al.*, 1995), *E. coli* (Blattner *et al.*, 1997), and yeast (*S. cerevisiae*) (Mewes *et al.*, 1997), and *D. melanogaster* (Adams *et al.*, 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, *C. elegans*, and *Arabidopsis sp.* Several databases containing genomic information annotated with some functional information are maintained by different organization, and are accessible via the internet, for example, The Institute for Genomic Research website [<http://www.tigr.org/tdb>]; the University of Wisconsin Laboratory of Genetics website [<http://www.genetics.wisc.edu>]; the Stanford genome website [<http://genome-www.stanford.edu/~ball>]; the HIV database website [<http://hiv-web.lanl.gov>]; the National Center for Biotechnology Information website [<http://www.ncbi.nlm.nih.gov>]; the European Bioinformatics Institute [<http://www.ebi.ac.uk>]; the Institut Pasteur website [<http://Pasteur.fr/other/biology>]; and the Whitehead Institute/MIT Center for Genome Research website [<http://www.genome.wi.mit.edu>].

Paragraph beginning at page 26, line 7 has been amended as follows:

One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, Nuc. Acids Res. 25:3389-3402, 1977, and Altschul *et al.*, J. Mol. Biol. 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information website [(http://www.ncbi.nlm.nih.gov/)]. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectations (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N= -4, and a comparison of both strands.

Paragraph beginning at page 27, line 24 has been amended as follows:

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid

sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine, *e.g.*, at the National Center for Biotechnology Information website [www.ncbi.nlm.nih.gov].

Paragraph beginning at page 119, line1 has been amended as follows:

NCBI, National Library of Medicine. National Institutes of Health: BLAST Sequence Similarity Searching (the National Center for Biotechnology Information website [web site = www.ncbi.nlm.nih.gov]).

In the claims:

Claims 1-17 and 19-40 are cancelled.

Claim 18 has been amended as follows:

18. (Twice Amended) A method to produce an animal feed containing a microbial phytase comprising:

a) providing [preparing] a plant cell, plant part or plant that contains a recombinant expression system comprising a phytase-encoding nucleic acid sequence having a nucleotide sequence selected from

- i) SEQ ID NO: 1, and
- ii) SEQ ID NO: 1, wherein T can also be U;

b) culturing the plant cell, plant part or plant under conditions wherein said nucleotide sequence is expressed as a polypeptide; and

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c) converting said plant cells, plant parts or plants into a composition suitable for animal feed, wherein the animal feed contains phytate and the phytase.

Claims 49-71 have been added.